

Please substitute the following for the paragraph beginning on page 4, line 21 and ending on page 4, line 28

C3 Fig. 3 is the nucleotide and deduced amino acid sequences (SEQ ID NO:4 and SEQ ID NO:6, 27, and 28, respectively) of the human protease-activated gene coding region cDNA. The deduced amino acid sequence is provided below the nucleotide sequence and contains 374 amino acids. The coding region of the cDNA sequence begins at nucleotides 58-60 (ATG = Met) and ends at nucleotides 1180-1182 (TAG = stop).

Please substitute the following for the paragraph beginning on page 4, line 31 and ending on page 5, line 5

C4 Fig. 5A shows the alignment of the deduced amino acid sequences (SEQ ID NO: 3, 6, 7, 8, 9, 24, 25, 26, 27 and 28) of the mouse PAR3, human PAR3, human PAR1, and human PAR2. To indicate homology, gaps (represented by blank spaces) have been introduced into the five sequences. Transmembrane domains are overlined (TM1-7). Fig. 5B shows the alignment of the hirudin-like portion of human PAR1, PAR2, and PAR3 amino acid sequences.

In the Claims

C5 6. (AMENDED) The substantially pure protein of claim 5 having an amino acid sequence selected from the group consisting of the sequence shown in Fig. 1 (SEQ ID NO:3, 24, 25, and 26) and the sequence shown in Fig. 2 (SEQ ID NO:6, 27, and 28).

7. (AMENDED) A substantially pure polypeptide having an amino acid sequence which is at least 80% identical to an amino acid sequence selected from the group consisting of the sequence shown in Fig. 2 (SEQ ID NO:3, 24, 25, and 26) and the sequence shown in Fig. 2 (SEQ ID NO:6, 27, and 28), wherein

a) said polypeptide is activated by thrombin; and

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Cont

b) said polypeptide mediates phosphoinositide hydrolysis in a cell expressing said polypeptide on its surface.
